

Spacing Between Adjacent Peaks in the Raw Data  
(M13, T's T=6% 60C, Long Gel)

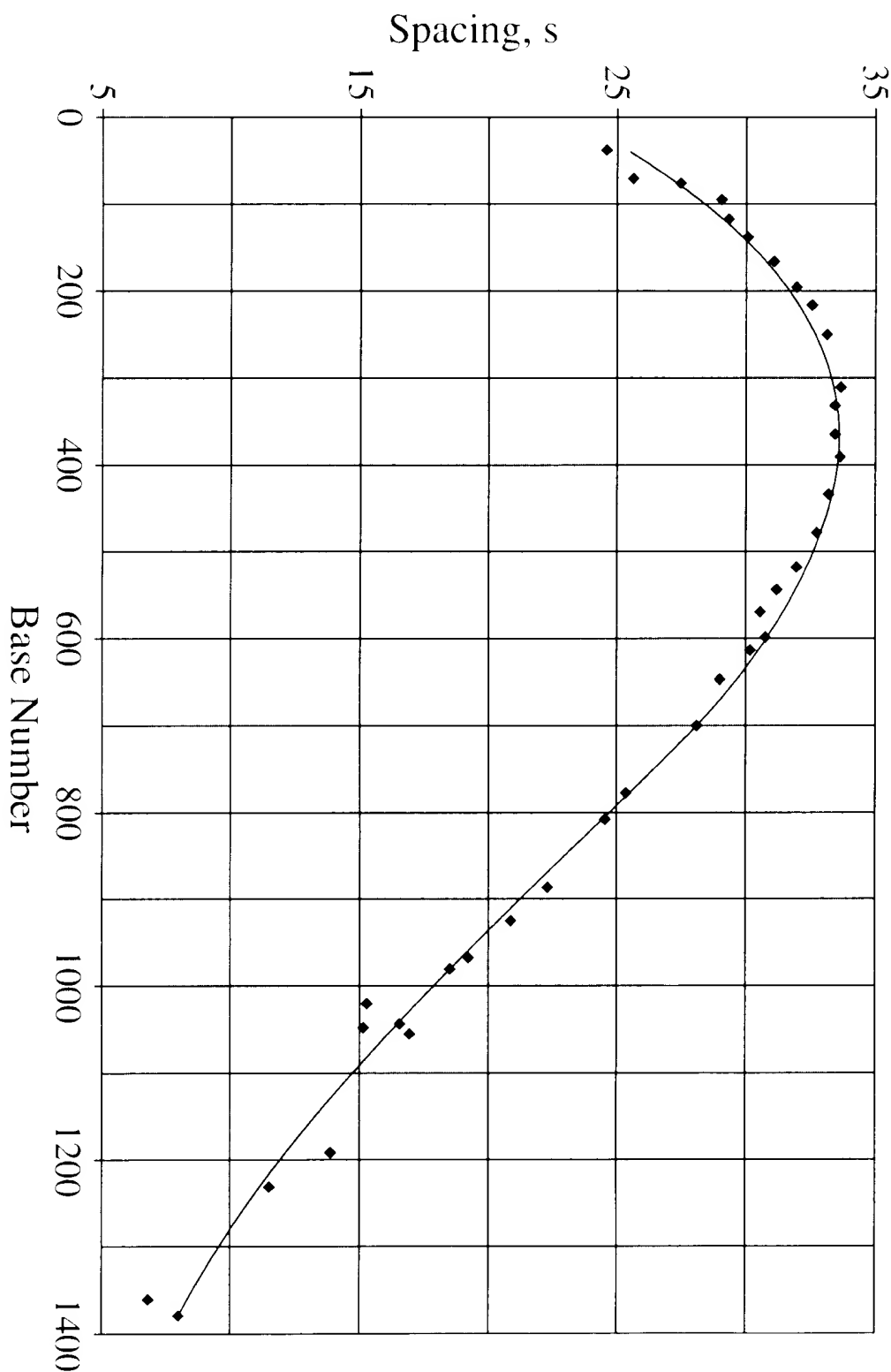


FIG. 1



Standard Deviation (%) of the Spacing Between Adjacent Bases from  
Average as a Function of Number of Peaks Used as a Reference for  
Alignment of Raw Data

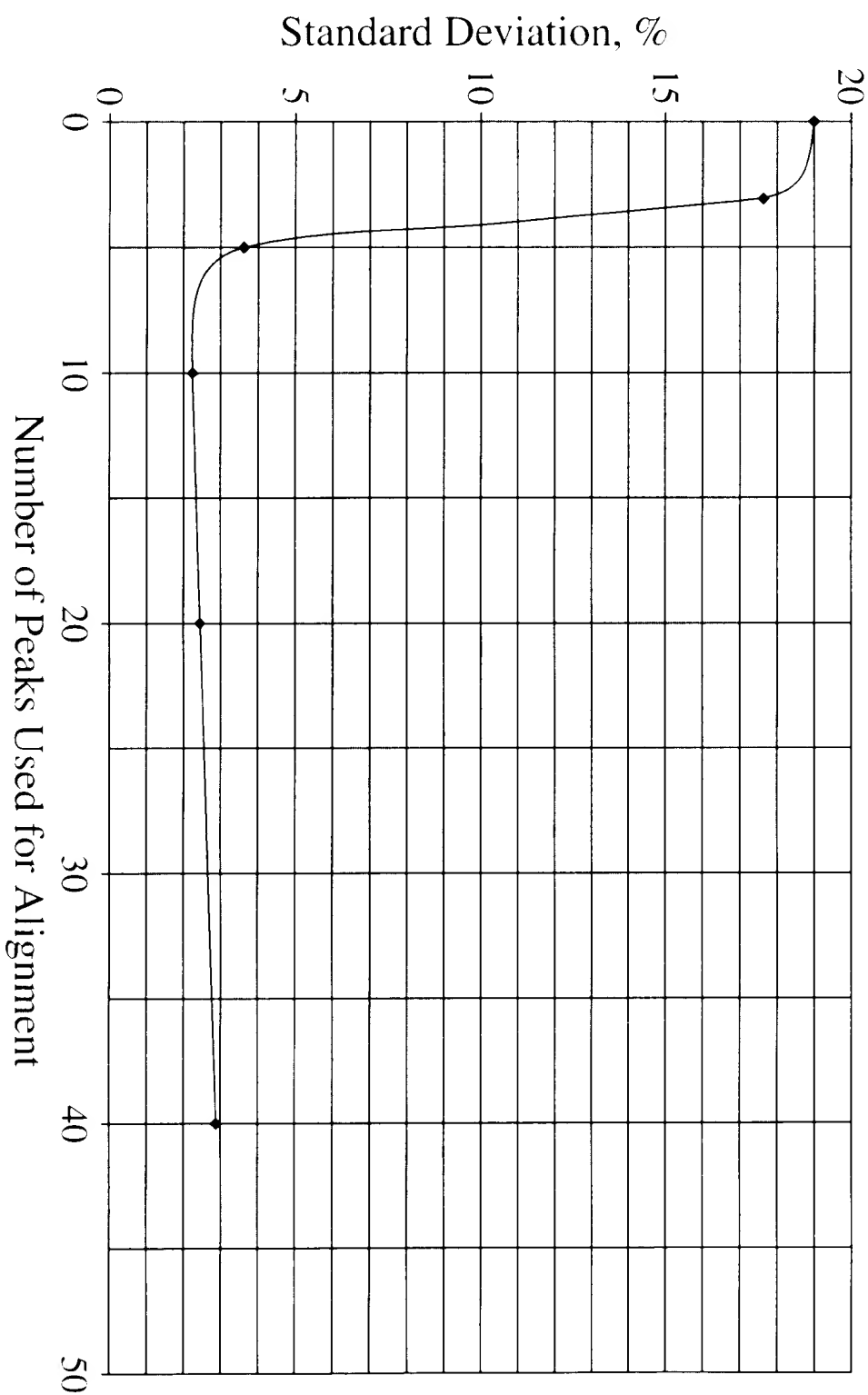


FIG. 3



4/14

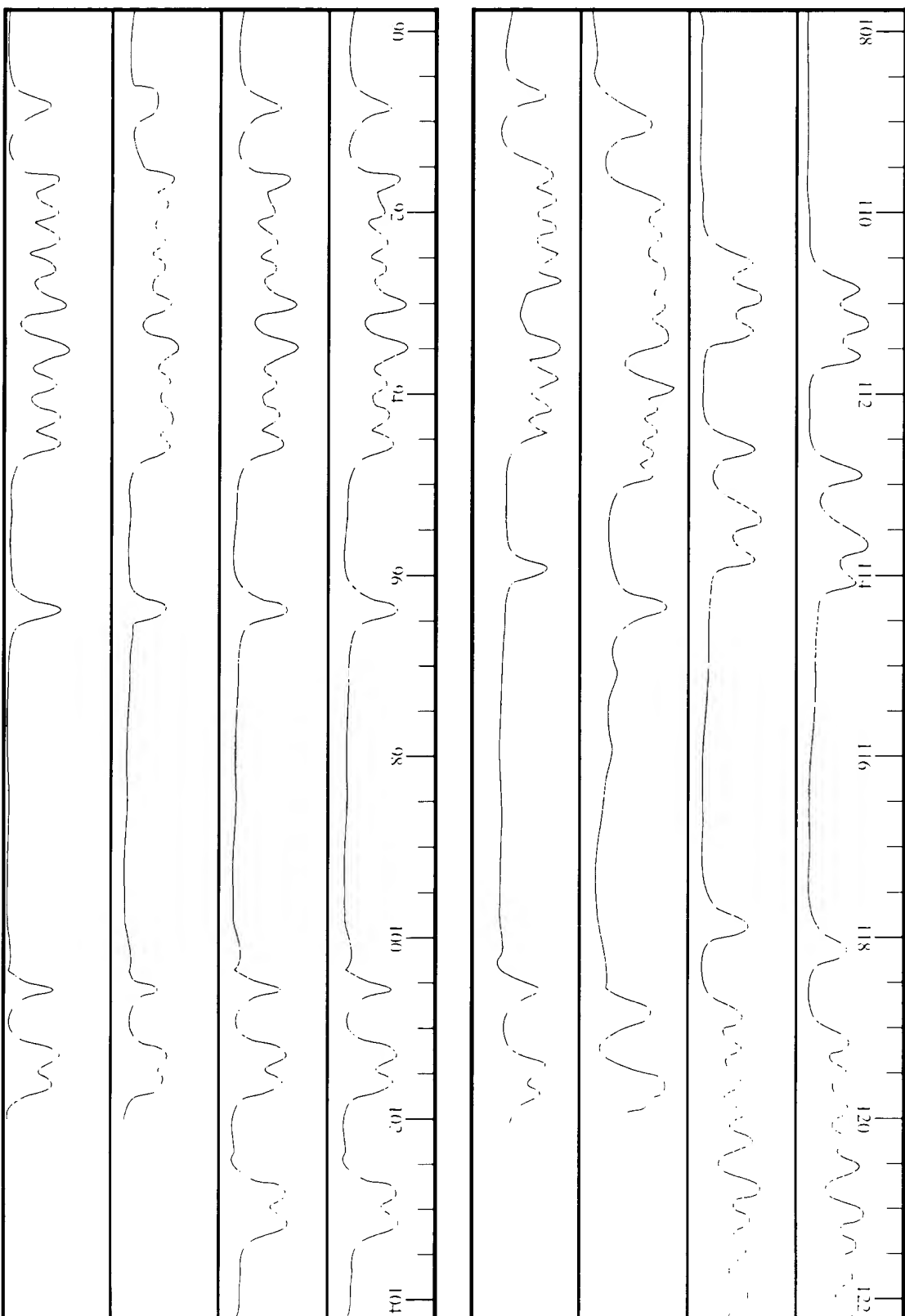
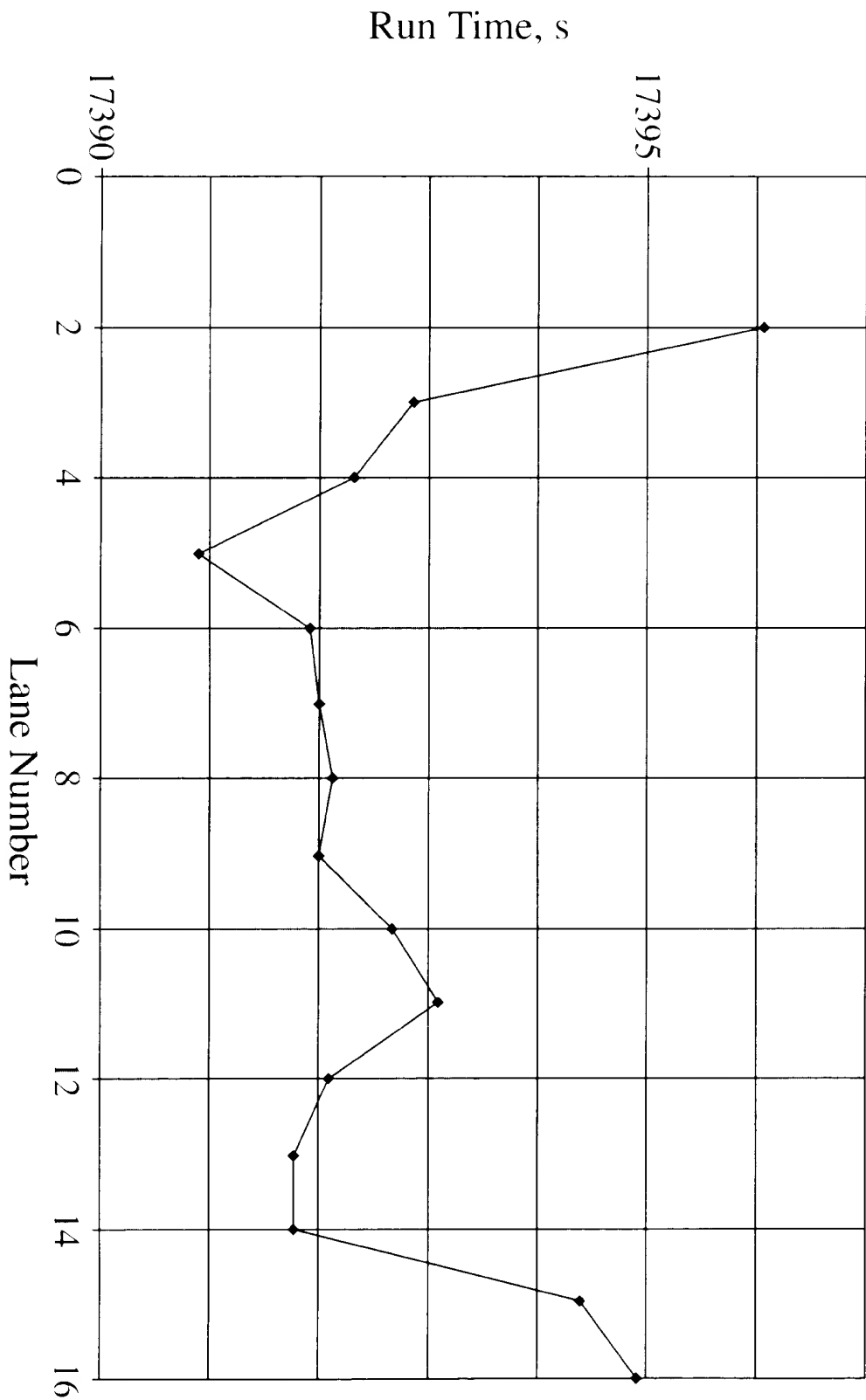


FIG. 4



5/14

**Run Time of the BP#1056 in Different Lanes  
(after alignment based on 10 peaks)**



**FIG. 5**

# HIV-1 TruGene Kit (version 0.80)

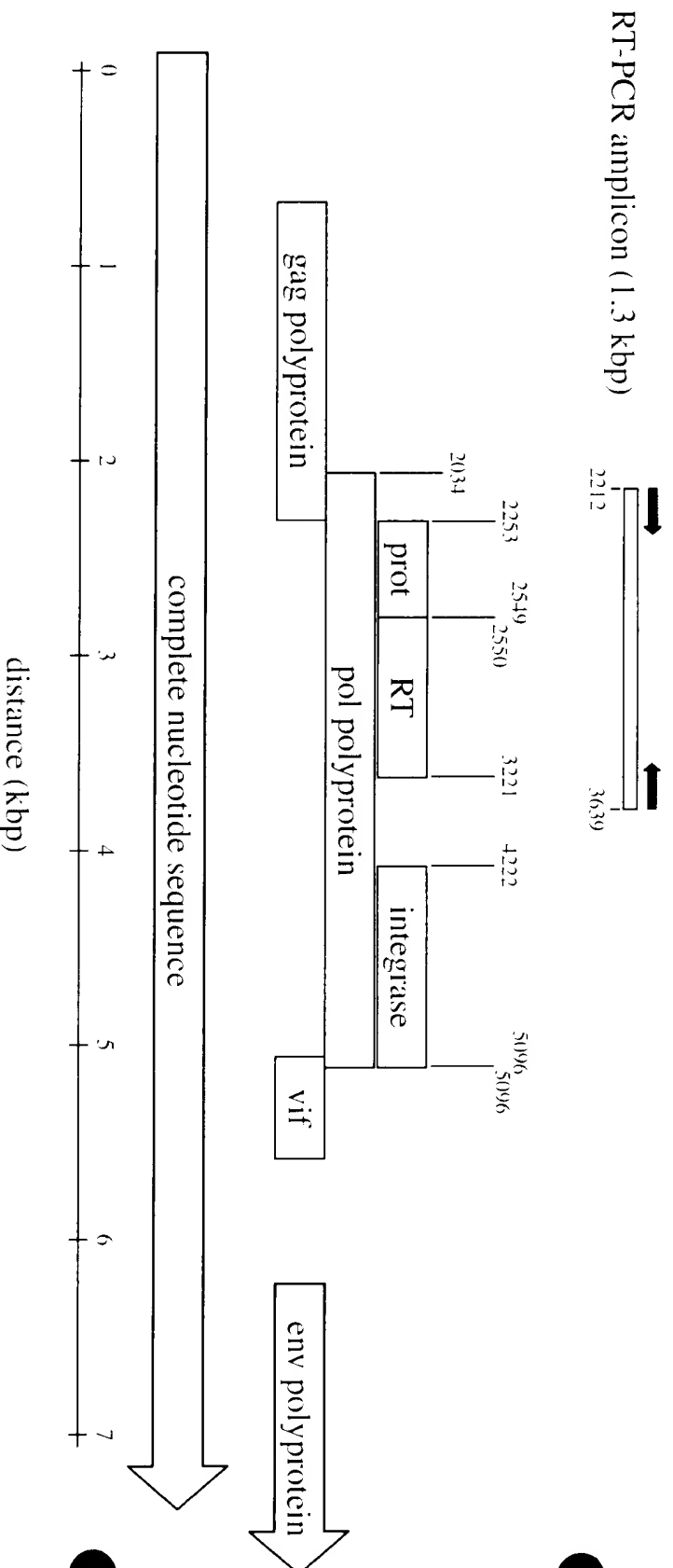


FIG. 6

## Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

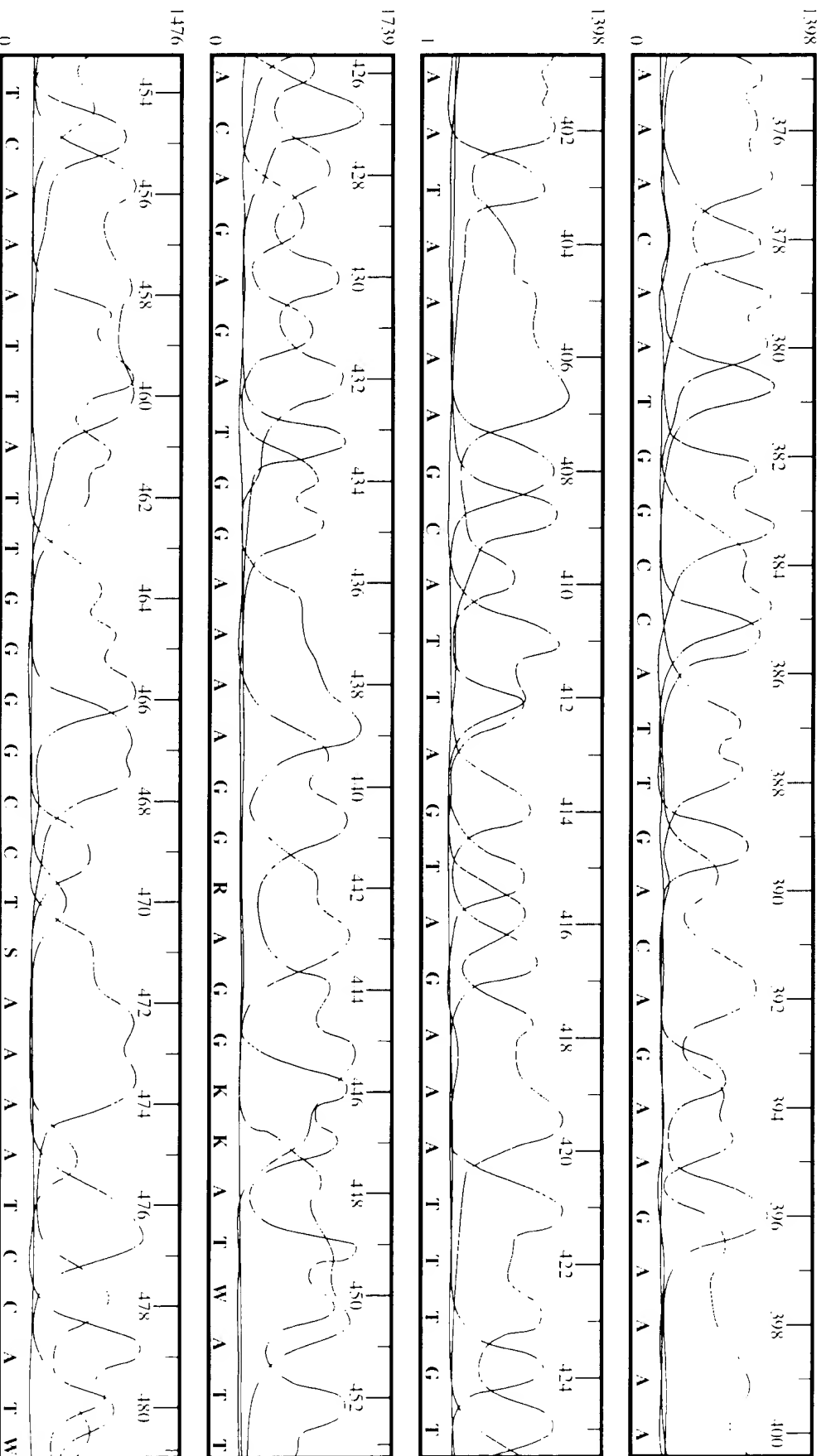
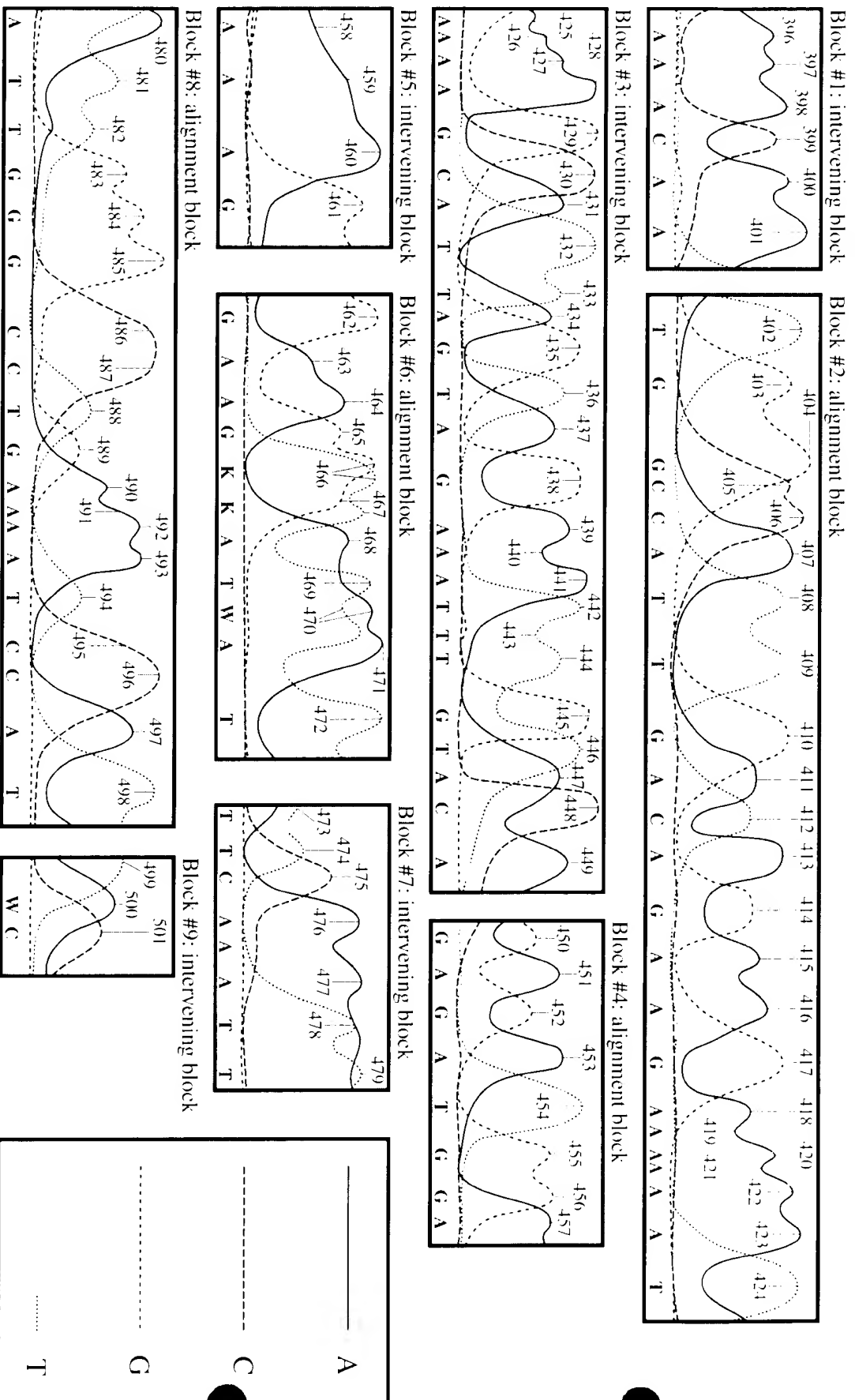


FIG. 7

# Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc



**FIG. 8**

# Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

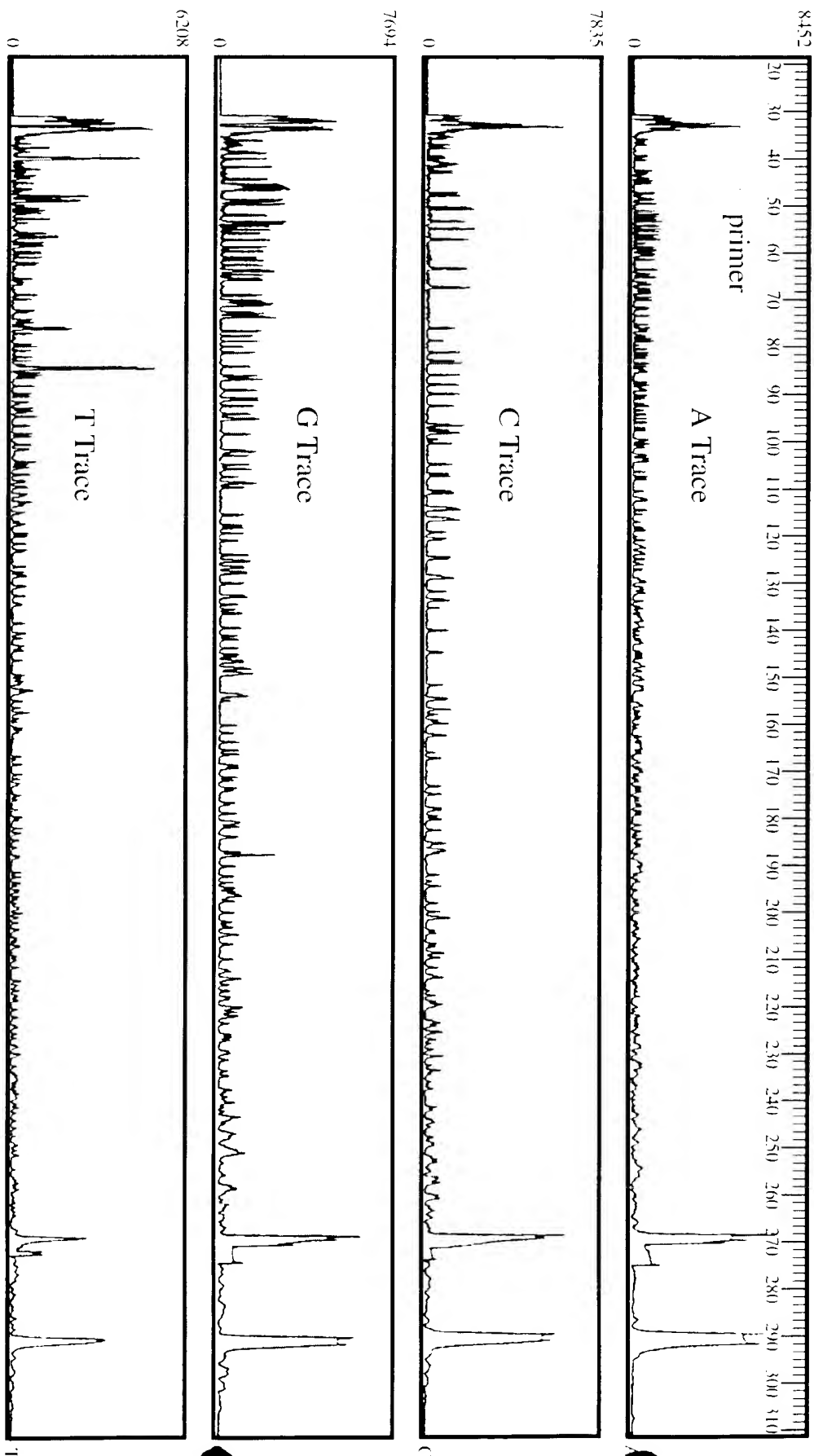


FIG. 9A





10/14

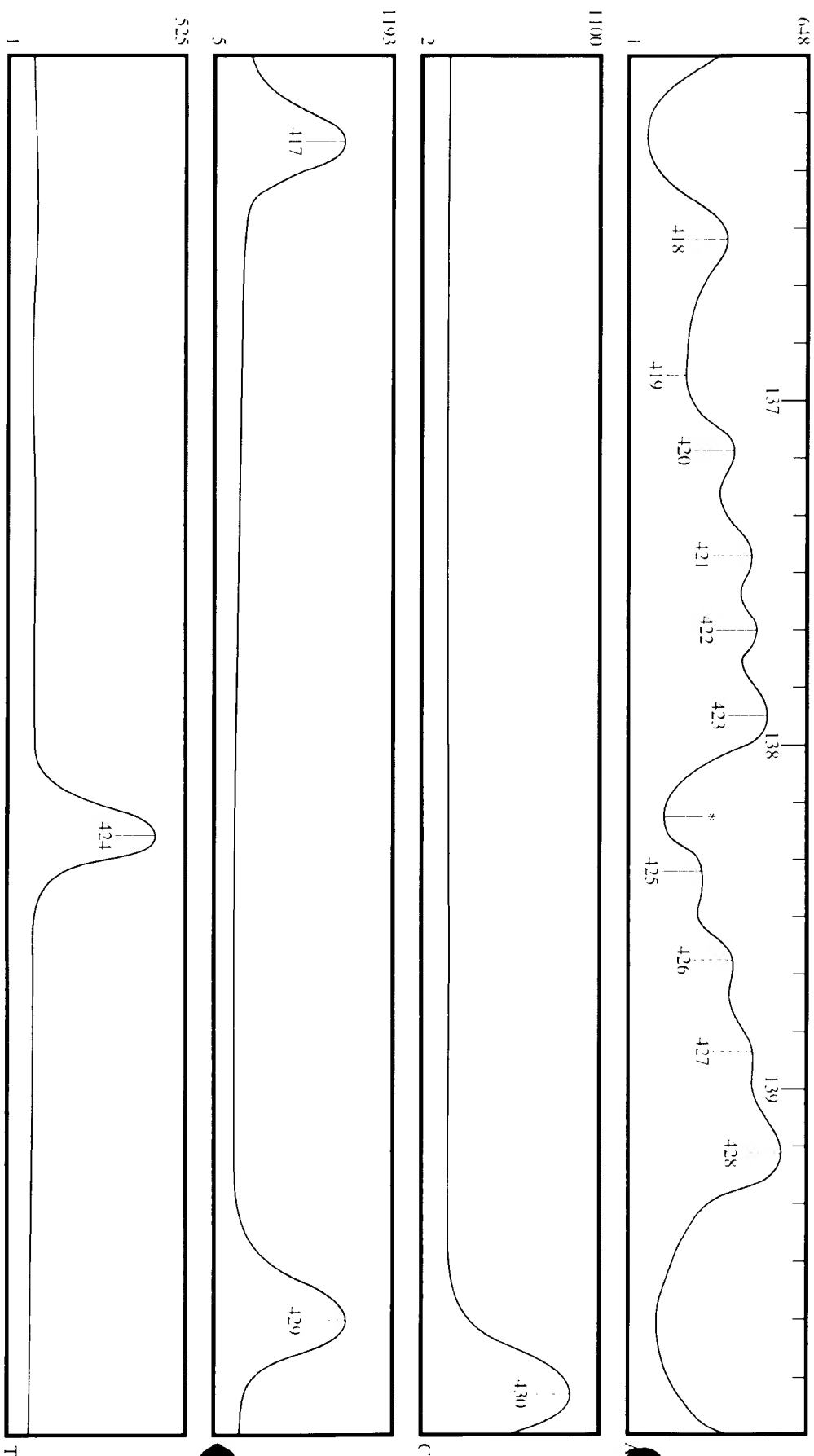


FIG. 9B



# Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

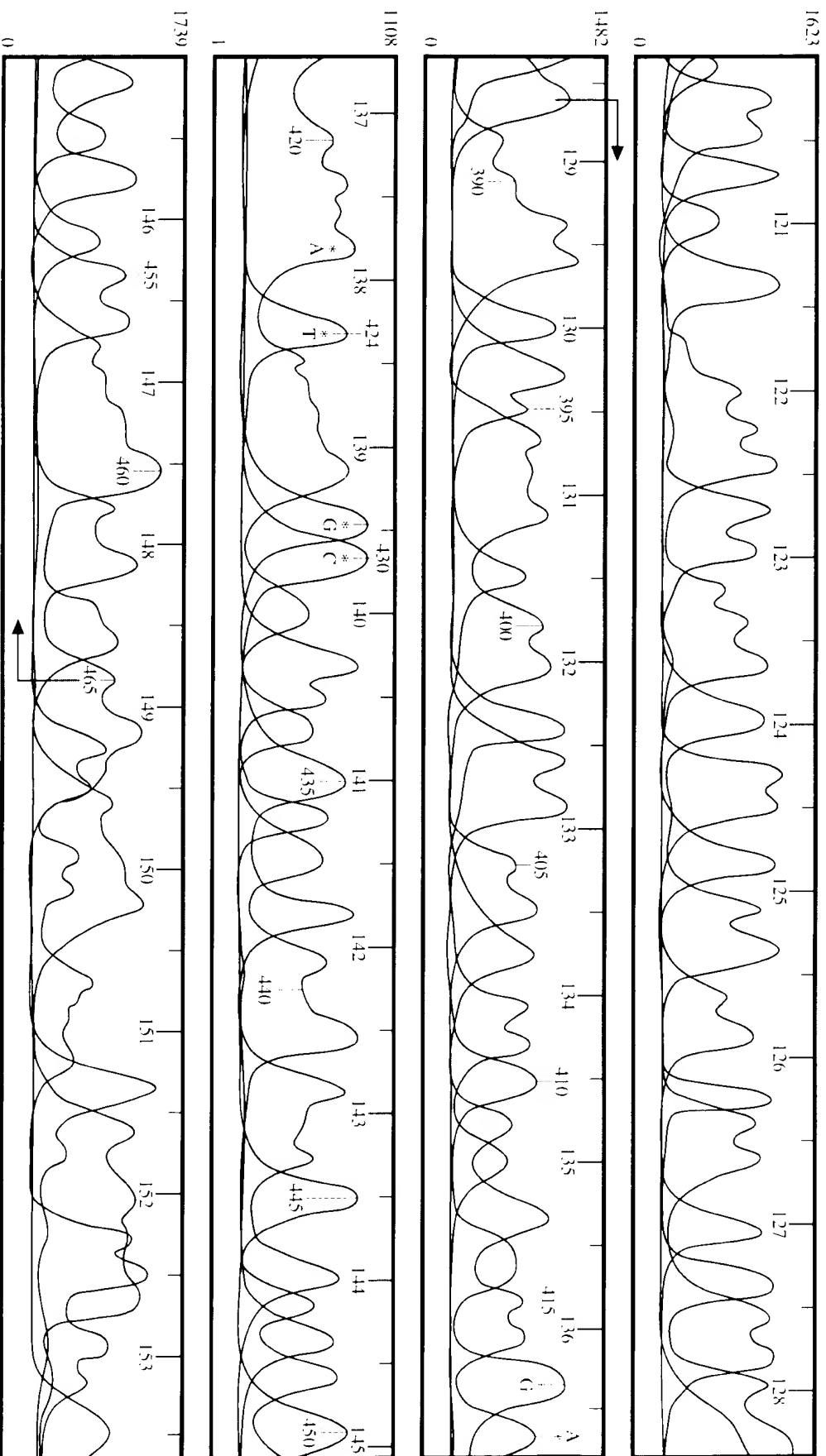


FIG. 9C

**FIG. 10**

**Deviation of the Peak Position from the Average as a Function  
of Base Number in the Traces Aligned with Internal Standards  
(long gel, M13, 6 peaks, 5-th degree polynomial)**

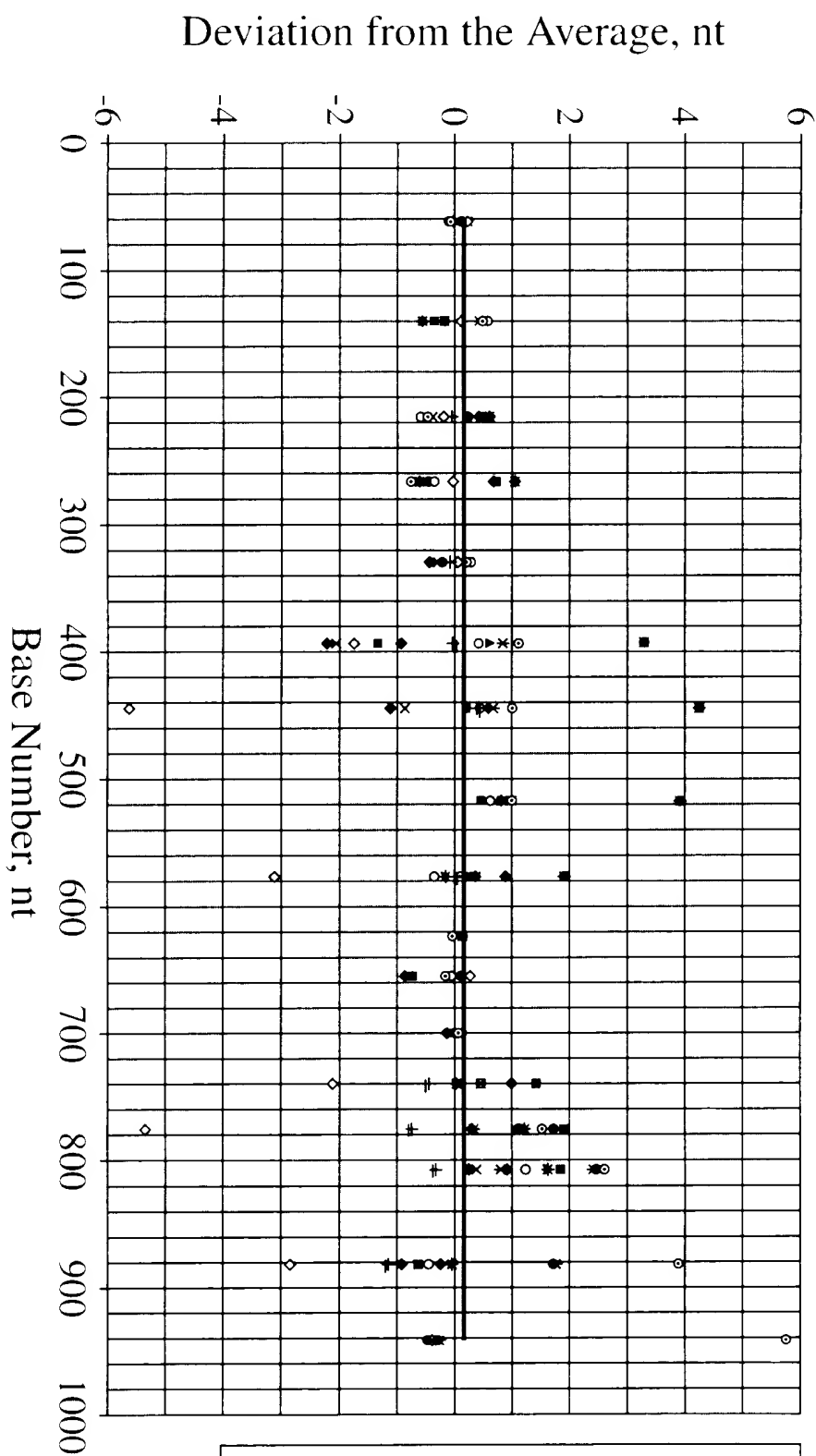


FIG. 12